We prepared all nucleosome constructs by mixing either c11 or g11 DNA together with either full length or recombinant histones octamers. The c11 DNA has four repeats of the 147 bp positioning sequence separated by 20 bp linker DNA. The sequence for the c11 DNA is as follows:

C11 (bp):

same prefix (9bp): ATCGAAGAC

different 1 (7bp): AGTACTG

same piece 1 (9bp): GCCGCCCTG

W601 (141bp): GAGAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 1 (7bp): AGTACTG

same piece 1 (9bp): GCCGCCCTG

W601 (141bp): GAGAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 1 (7bp): AGTACTG

same piece 1 (9bp): GCCGCCCTG

W601 (141bp): GAGAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 1 (7bp): AGTACTG

same piece 1 (9bp): GCCGCCCTG

W601 (141bp): GAGAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

Almost same piece 2 (7bp): TGTGCAT...

different suffix (10bp): TAAGTACTCT

same suffix (9bp): GTCTTCGAT

G11 (bp):

same prefix (9bp): ATCGAAGAC

different 1 (10bp): GTCTTACGCG

same piece 1 (9bp): GCCGCCCTG

almost W601 (141bp):

GACAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 2 (17bp): TTGAAAGTACTTACGCG

same piece 1 (9bp): GCCGCCCTG

almost W601 (141bp):

GACAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 2 (17bp): TTGAAAGTACTTACGCG

same piece 1 (9bp): GCCGCCCTG

almost W601 (141bp):

GACAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different 2 (17bp): TTGAAAGTACTTACGCG

same piece 1 (9bp): GCCGCCCTG

almost W601 (141bp):

GACAATCCCGGTGCCGAGGCCGCTCAATTGGTCGTAGACAGCTCTAGCACCGCTTAAACGCACGTACGCGCTGTCCCCCGCGTTTTAACCGCCAAGGGGATTACTCCCTAGTCTCCAGGCACGTGTCAGATATATACATCC

same piece 2 (10bp): TGTGCATGTA

different suffix (15bp): TTGAAAGTACTTAGA

same suffix (9bp): GTCTTCGAT

The Widom 601(W601) sequence, shown to bind octamers from *Xenopus laevis* in a localized manner*,* is highlighted in grey. The G11 sequence has 1 bp variation from the Widom 601 sequence shown in red. Both C11 and G11 have the same sequence which totals 19bp (shown in teal) before and after each Widom 601 sequence with the only exception being the forth such sequence of the C11 where 3 bp are missing (shown in magenta). Between these sequences, the linker DNA sequence is shown in green. This linker sequence for the G11 is 10 bp longer than that of the C11. *At the beginning and end of both the G11 and C11, there is an outer section that is identical between the C11 and G11 (shown in orange) with an inner section that differs (shown in yellow).* The ScaI-HF enzyme cut sequence, AGT¦ACT, is highlighted in neon green to illustrate where the DNA will be digested by this enzyme. As a measure of array quality ScaI-HF is used to digest the tetramer into individual nucleosomes, each with

The G11 has a total length of 734 bp while the C11 has a total length of 693. Each nucleosome octamer binds 147bp of DNA, the 141bp of the W 601 section as well as the 3bp before and after. This means that the C11(G11) will have a 22bp (25bp) prefix, 20bp (30bp) linker, and 23bp (31bp) suffix.

As a note, the EcoRV-HF enzyme cuts DNA at GAT’ATC and the ScaI-HF enzyme cuts DNA at AGT’ACT. Using this enzyme, the C11 tetramer complex will be cut into 3 nucleosomes with 167bp and 1 nucleosome with 166bp dsDNA attached, while the G11 tetramer complex will be cut into 1 nucleosome with 187bp and 3 nucleosomes with 177bp dsDNA attached.